
بسم الله الرحمن الرحيم
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Medical Biotechnology group
School of Paramedical Sciences
Qazvin University of Medical Sciences

Introduction to microRNAs

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Contents

MicroRNA

- small, non-protein-coding RNA molecules~ 22 nucleotides(1)
- regulate gene expression by inhibiting translation and/or by inducing degradation of target mRNAs(2)
- Repress activity of complementary mRNAs(1)
- 1 miRNA = hundreds of mRNAs (1)

MicroRNA

- The human genome may encode over 1000 miRNAs (1)
- Regulate 60% of mammalian gene products(1)
- They have been identified to play a key role in organ development, cellular differentiation, proliferation and function(1)
- Have been described in invertebrates and vertebrates: worms, fungi, plants, and mammals(1)

History of miRs

- In **1987**,Fergunsson *et al, found that* lin-4 could negatively regulate lin-14(3)
- In **1989**, Ambros focus his research on lin-4 gene and Ruvkun on the study lin-14 gene.(4)
- In **1992** Ambros and Ruvkun : lin-4 transcripts were complementary to a repeated sequence in the 3′UTR of lin-14 gene. (5)

History of miRs

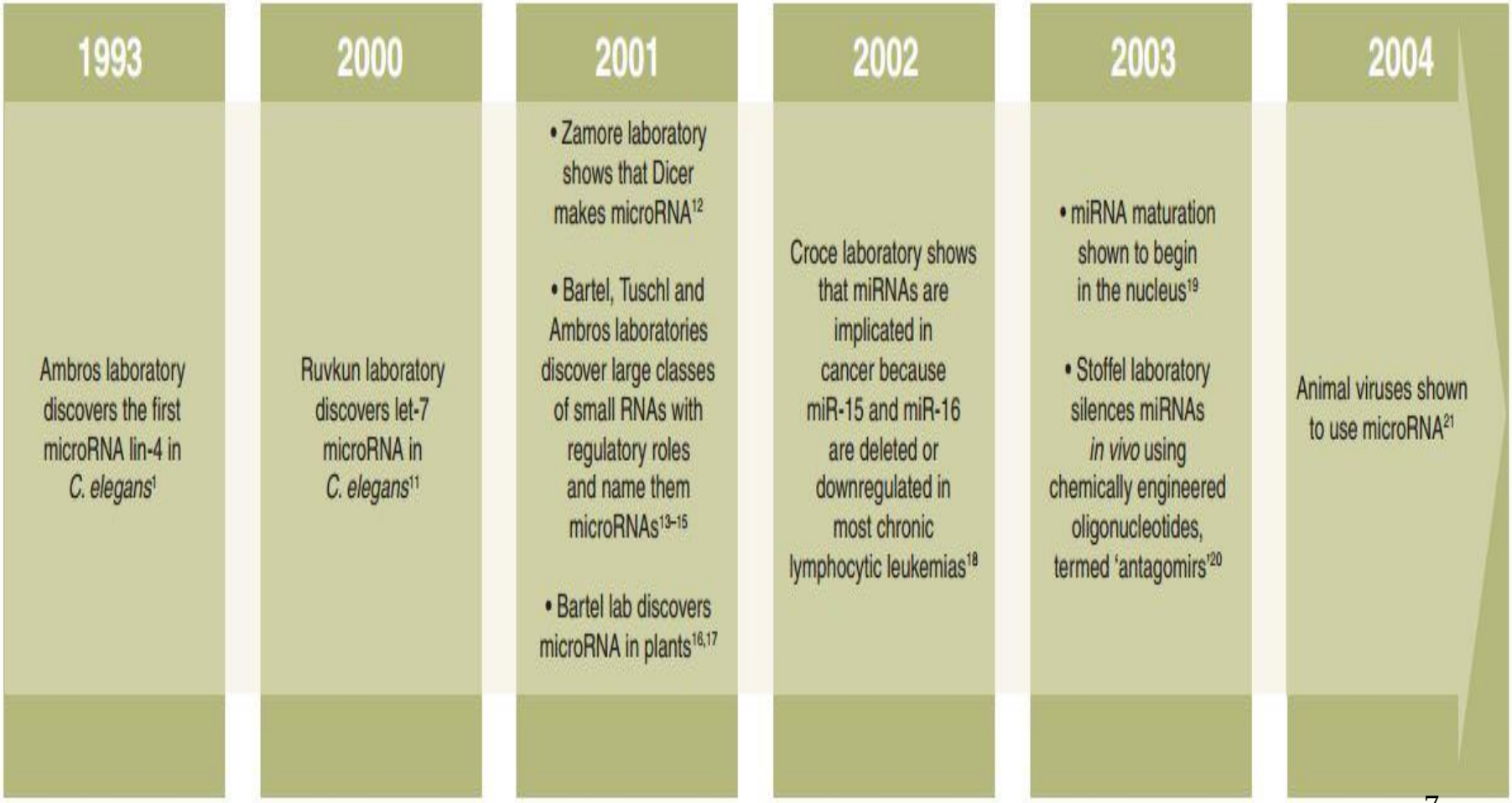
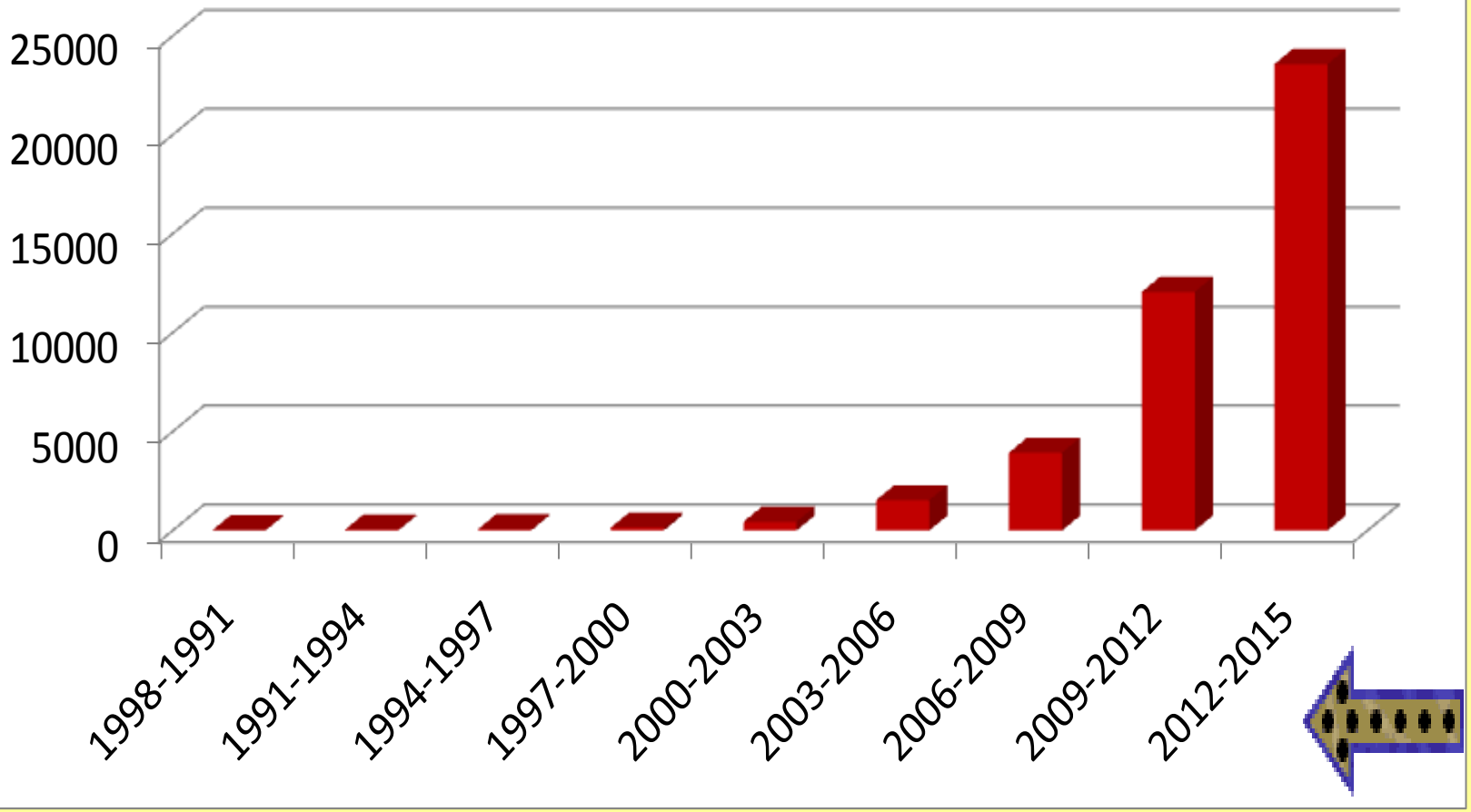


Figure 1 Milestones in miRNA research.

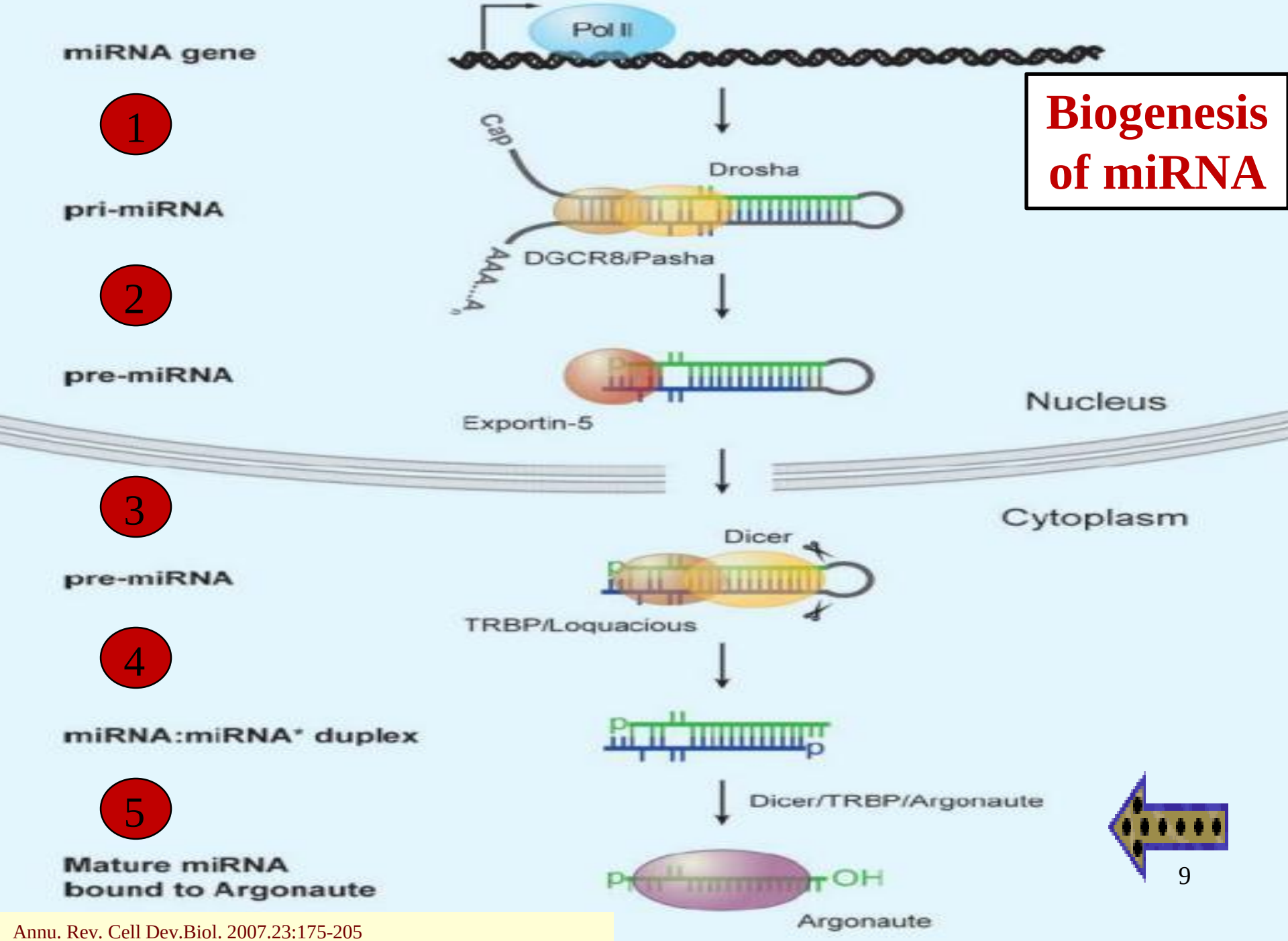
Mack GS. Nature biotechnology. 2007;25(6):631-8.

Published Articles of MicroRNA



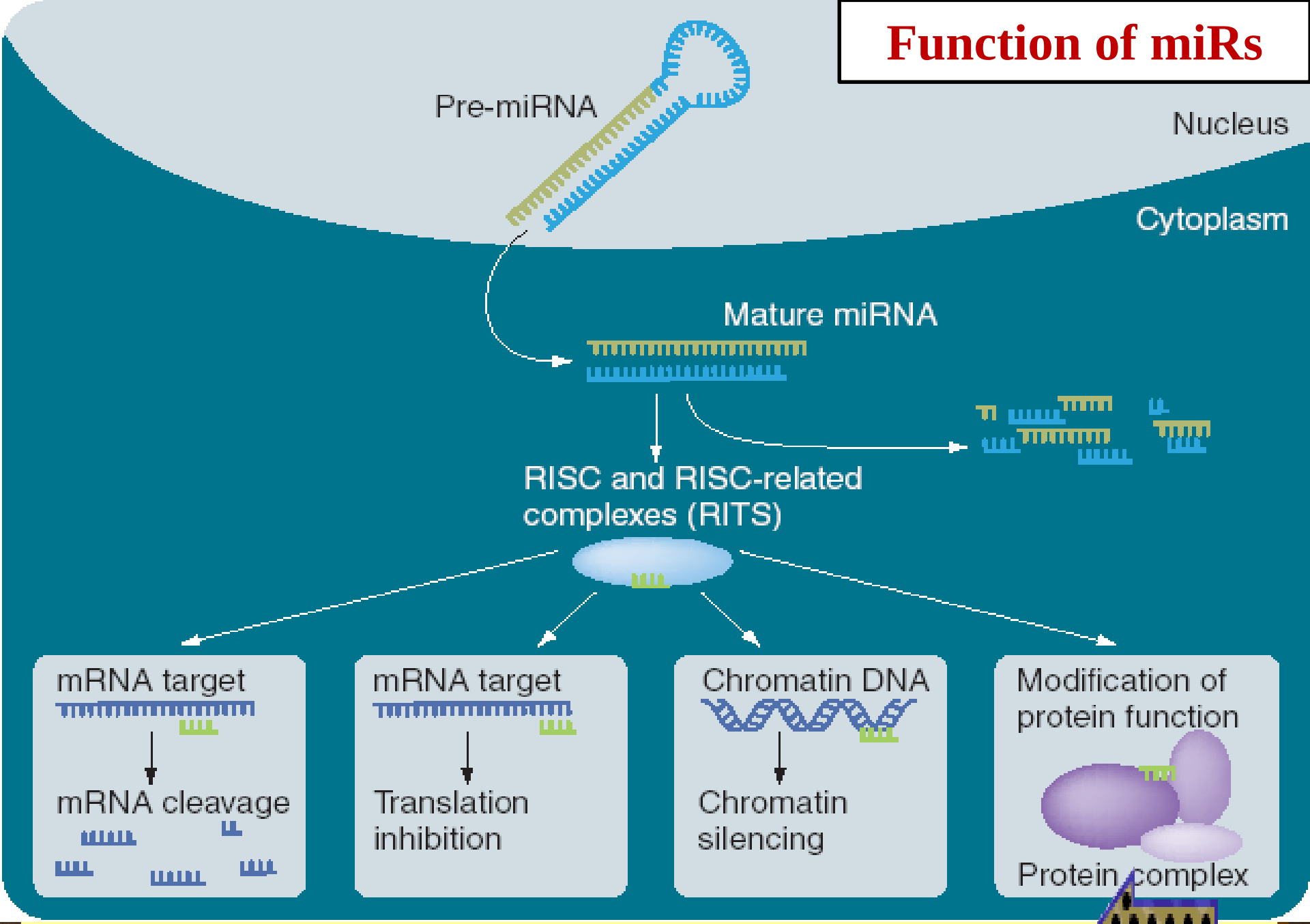
Retrieved from www.ncbi.nlm.nih.gov/pupmed,10 november 2015

Biogenesis of miRNA



Annu. Rev. Cell Dev.Biol. 2007.23:175-205

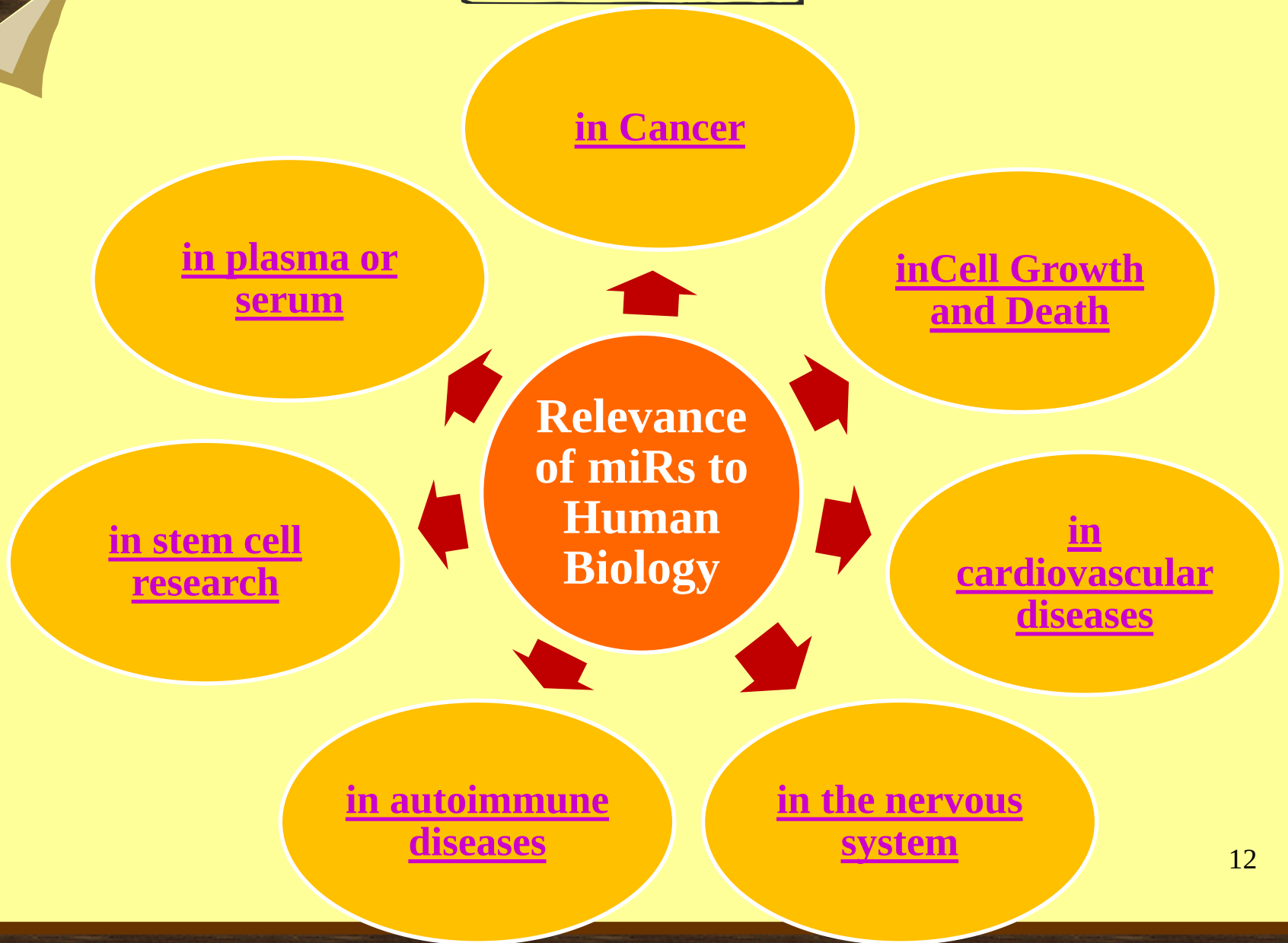
Function of miRs



Expert Rev. Mol. Diagn. 2007, 7(5) 569-603

Named miRs

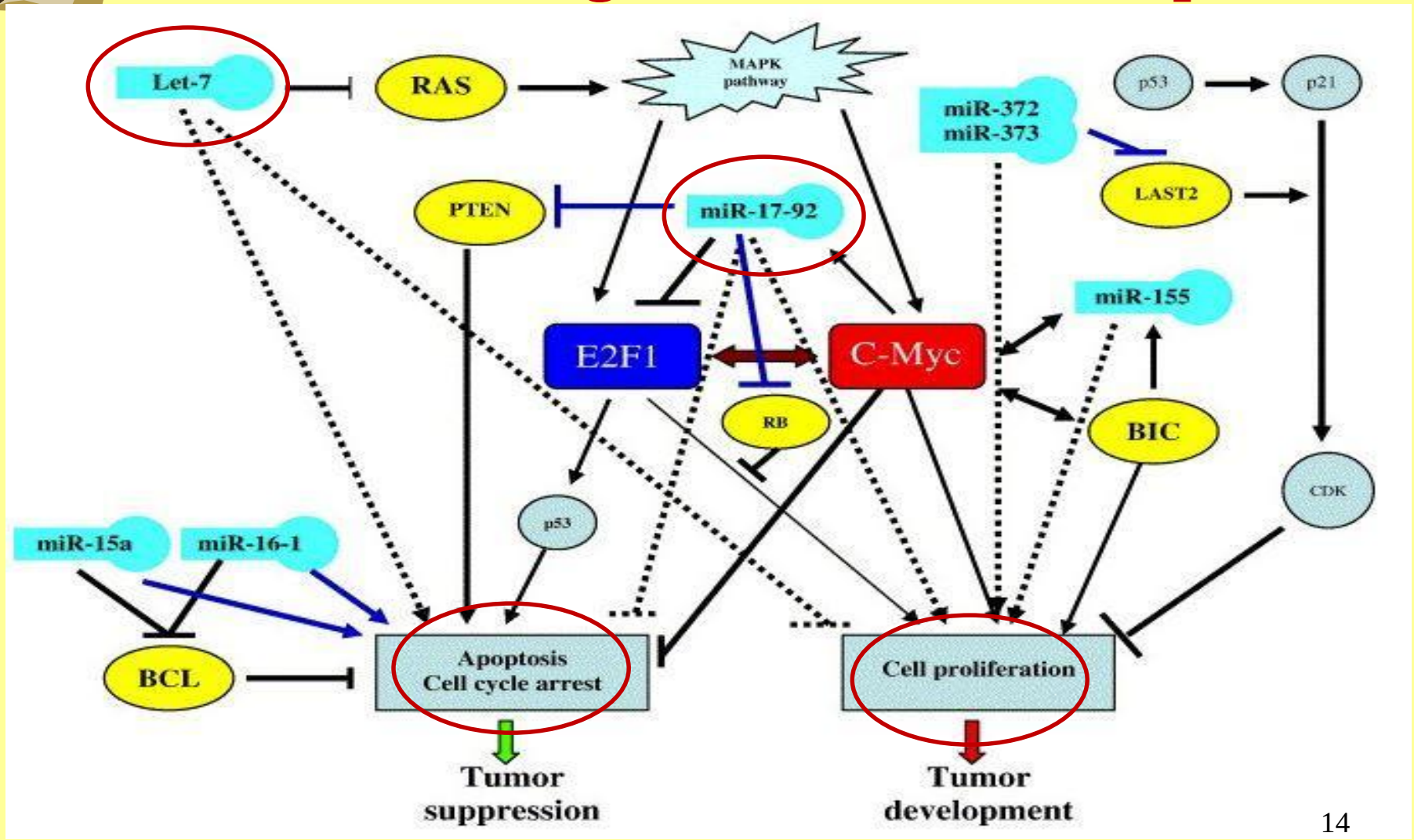
- ✓ hsa-miR-100 → Homo sapiens
- ✓ dme-miR-100 → Drosophila melanogaster
- ✓ miR-15-5p
- ✓ miR-15-3p*
- ✓ miR-181a
- ✓ miR-181b(6)


Relevance of miRs to Human Biology
in Cancer
inCell Growth and Death
in cardiovascular diseases
in the nervous system
in autoimmune diseases
in stem cell research
in plasma or serum

microRNAs in Cancer

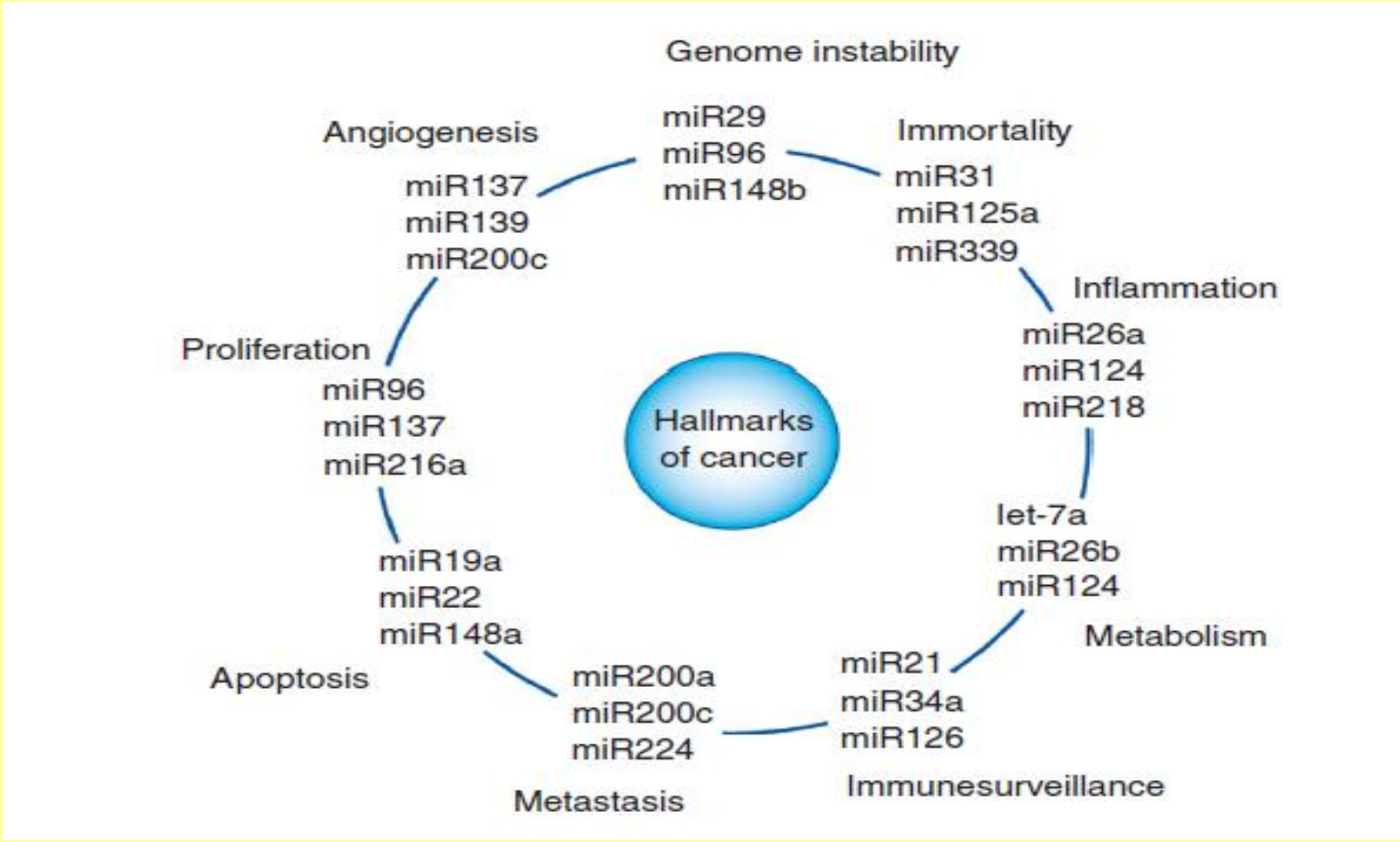
- **In 2002**, the first report ,miR-15 , miR-16 were found to be located at chromosome 13q14, a region frequently deleted in CLL (7)
- **In 2005,** MicroRNAs can act as oncogenes or tumor suppressors(8)
- **In 2006,** Saito et al. controlled by : DNA methylation , histone modifications(9)

miRNAs as Oncogenes and Tumor Supressors



Zhang et al Dev Biol. 2007 Feb 1;302(1):1-12

microRNAs in Cancer



Pichler M, Calin G.British journal of cancer. 2015;113(4):569-73.

microRNAs in Cancer

Table 1. Examples of important studies that implicated microRNAs in cancer diagnosis, prognosis and prediction of response to cancer drugs

Purpose	MicroRNA(s)	Type of cancer	Sample	Authors
Early detection	13 microRNA panel ('miR-Test')	Lung cancer	Serum	Montani *et al*, 2015
Diagnosis	24 microRNA panel	Kidney cancer	Tissue	Spector *et al*, 2013
Diagnosis	3 microRNA panel (miR21, miR31 and miR210)	Lung cancer	Sputum	Xing *et al*, 2015
Diagnosis	3 microRNA panel (miR200c, -93-3p, -192)	Mesothelioma	Tissue	Benjamin *et al*, 2010
Diagnosis	8 microRNA panel (miR106a, -125a-5p, -129-3p, -205, -21, -29b, -375, -7)	Lung cancer	Tissue	Gilad *et al*, 2012
Diagnosis	64 microRNA panel	Cancer of unknown primary	Tissue	Meiri *et al*, 2012
Diagnosis	48 microRNA panel	Cancer of unknown primary	Tissue	Rosenfeld *et al*, 2008
Prognosis	miR224	Colorectal cancer	Tissue	Ling *et al*, 2015
Prognosis	miR200a	Colorectal cancer	Tissue	Pichler *et al*, 2014
Prognosis	let-7i, miR-10b, miR-885-5p	Colorectal cancer	Tissue	Hur *et al*, 2015
Prognosis	miR155	Lymphoma	Cells	Iqbal *et al*, 2015
Prediction	miR212	Head and neck cancer	Tissue	Hatakeyama *et al*, 2010
Prediction	let7-binding site in KRAS gene	Colorectal cancer	Tissue or blood	Zhang *et al*, 2011

Pichler M, Calin G. British journal of cancer. 2015;113(4):569-73.

microRNAs in Cancer

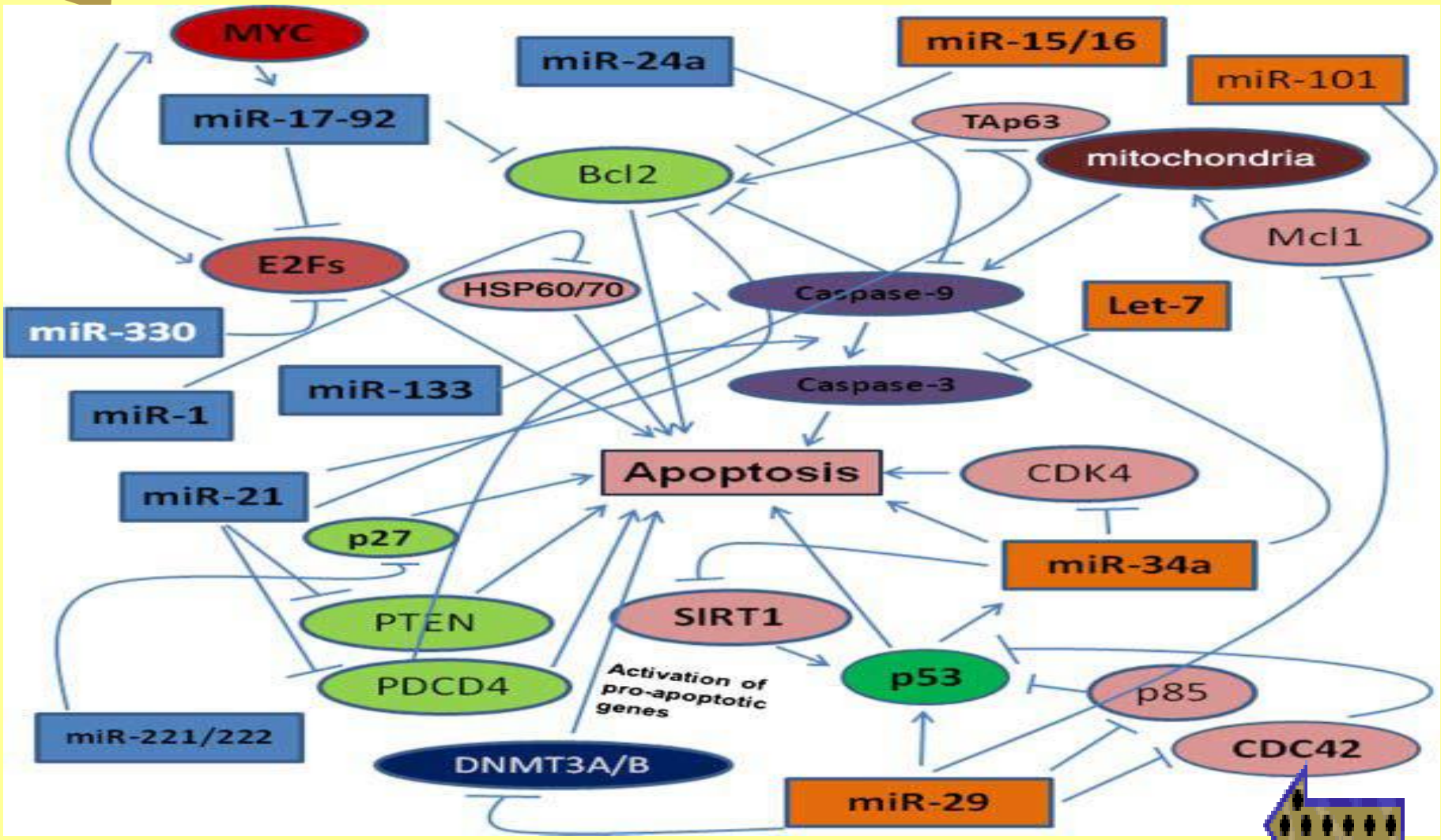
in 2015

Ferracin M et al

miR-181a-5p as a diagnostic

breast cancer biomarker(10).

miRNAs Regulate Cell Growth and Death



microRNAs in cardiovascular diseases

- **In 2005**, Zhao et al.miR-1-1,miR-1-2 were specifically expressed in cardiac and skeletal muscle precursor cells(11).
- **In 2006**, Rooij et al. microarray analysis,more than 12 miRNAs were cardiac hypertrophy and heart failure (12).
- **In 2010**,Edwards et al. several studies demonstrated miRNA aberrant patterns in cardiac hypertrophy and analyzed their roles(13).

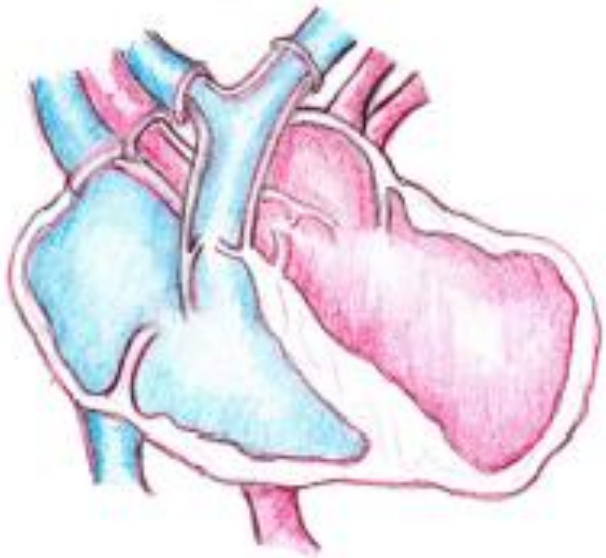
microRNAs in cardiovascular diseases

Normal Heart

miR-18b*	miR-129-5p	miR-499
miR-21	miR-133a	miR-519e*
miR-22	miR-142-3p	miR-520d-5p
miR-29b	miR-200b	miR-622
miR-30a	miR-210	miR-675
miR-92b	miR-320a	miR-1254
miR-122	miR-423-5p	HS_202.1

Diagnosis of Heart Failure

miR-30b	miR-125b	miR-142-5p
miR-103	miR-126	miR-342-3p
miR-107	miR-139	miR-497
	miR-142-3p	



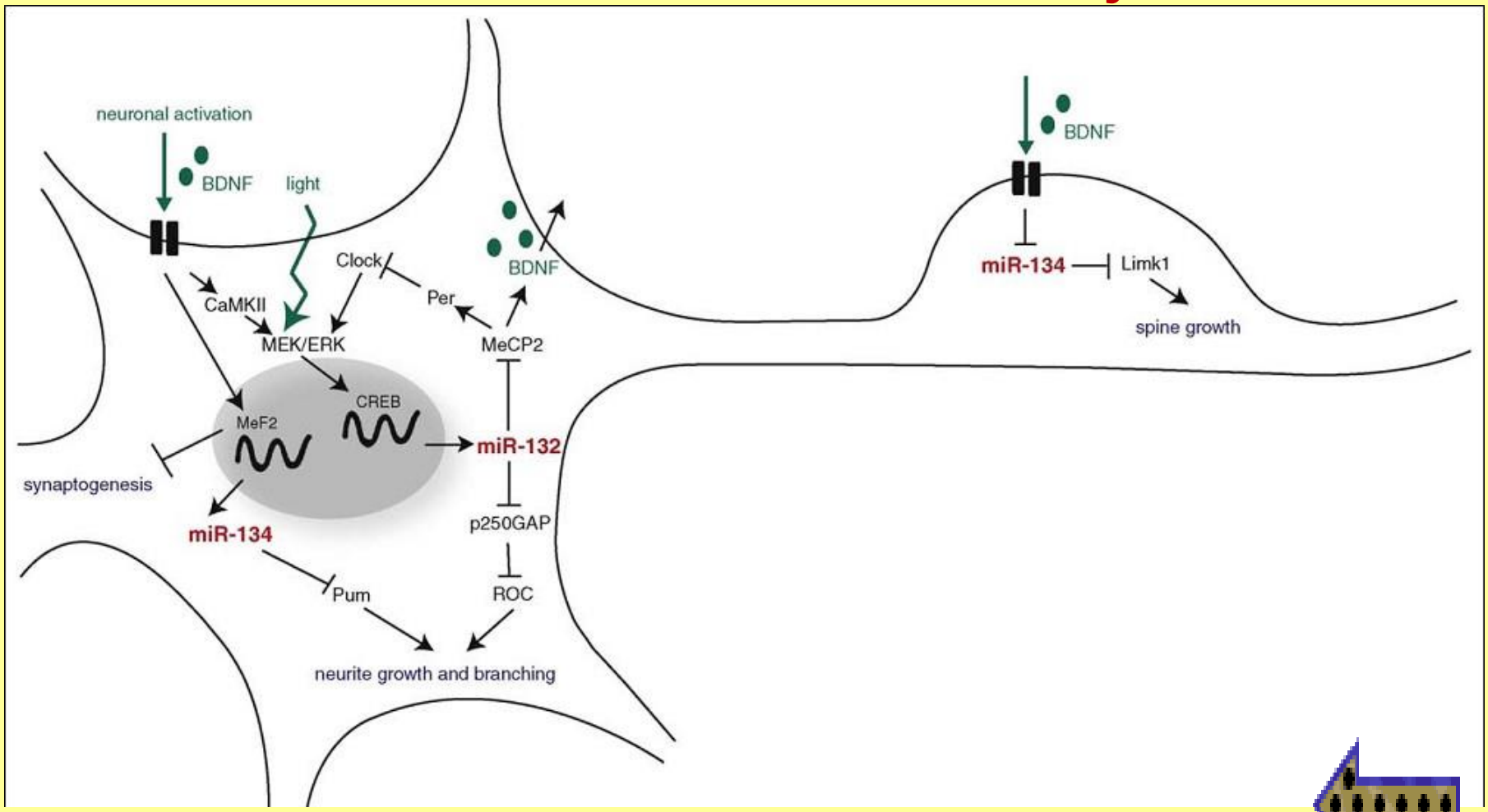
Heart Failure

Romaine SP, Tomaszewski M, Condorelli G, Samani NJ.. 2015;101(12):921-8.

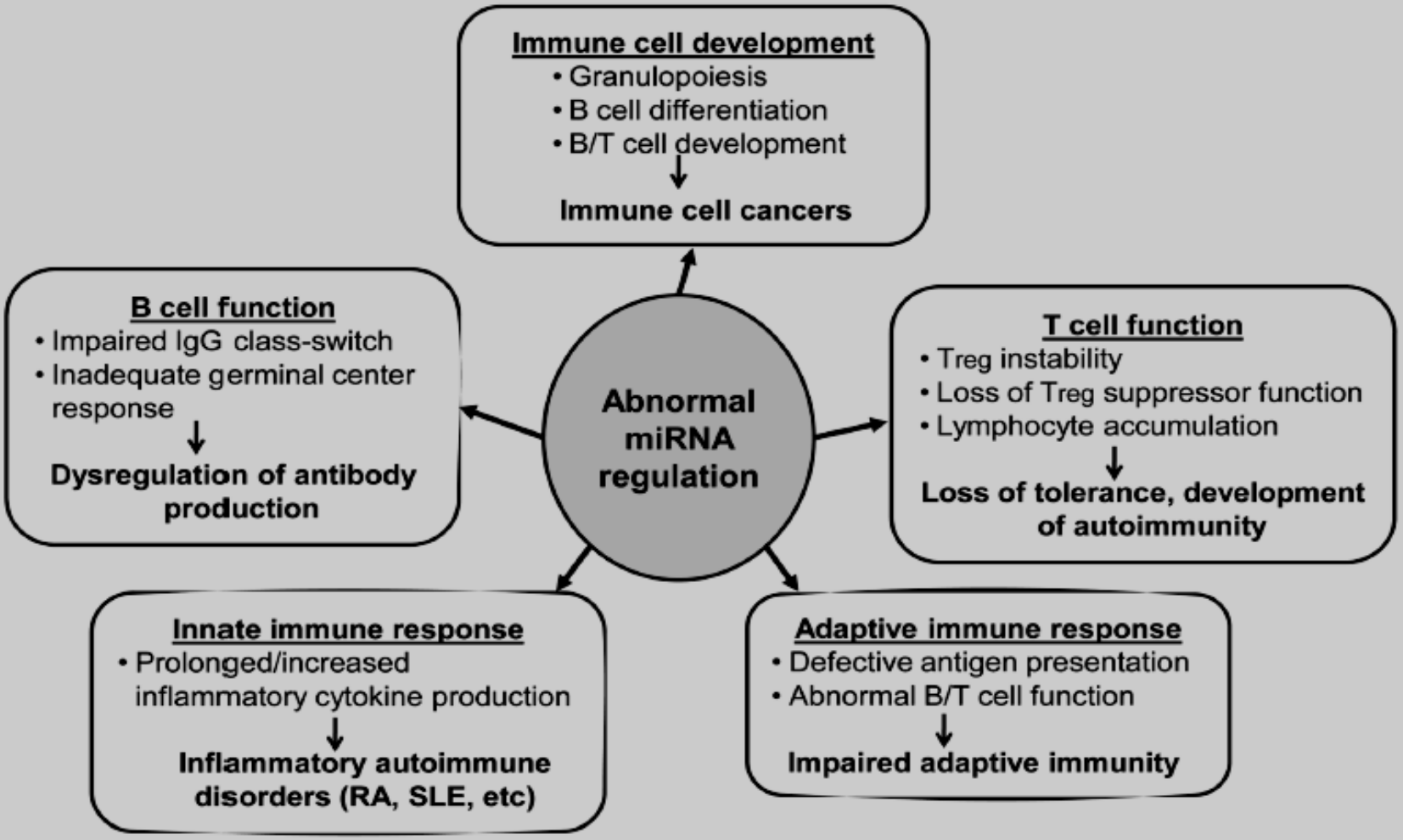
microRNAs in the nervous system

- key regulators of CNS development
  - involving brain plasticity
  - neuronal cell maturation
  - neuronal cell differentiation
  - synaptogenesis
- Dysregulation → Alzheimer, Parkinson, Huntington (14)

microRNAs in the nervous system



microRNAs in autoimmune diseases



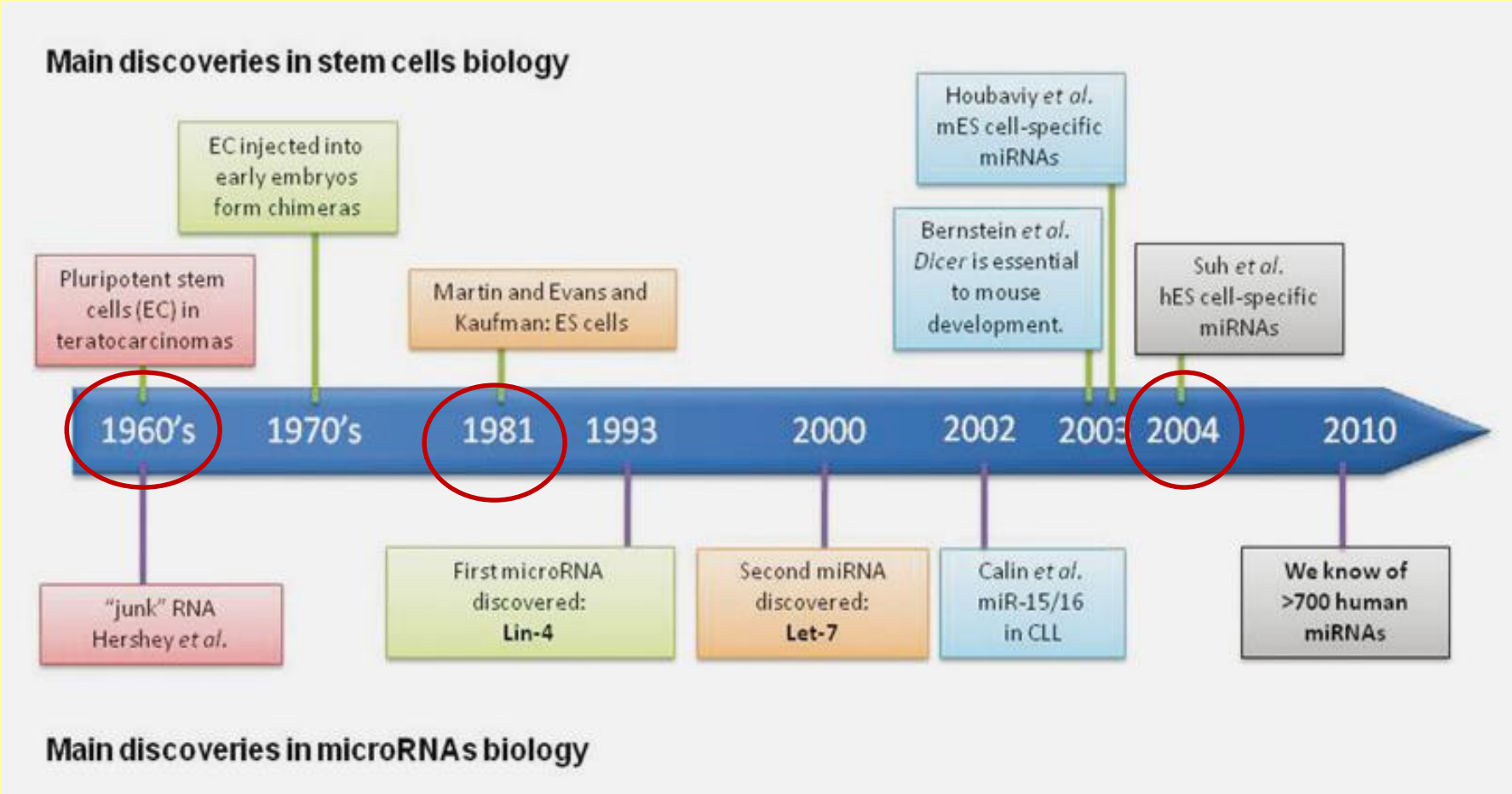
Pauley KM, Cha S, Chan EK. Journal of autoimmunity. 2009;32(3):189-94

microRNAs in autoimmune diseases

Diseases	Serum miRNAs	Expression levels
SLE	MiR-146a	↓
	MiR-155	↓
	MiR-200a	↓
	MiR-342-3p, MiR-223, and MiR-20a	↓
	MiR-142-3p	↓
	MiR-126	↑
PS	MiR-369-3p	↑
SSc	MiR-29a	↓
	MiR-196a	↓
	MiR-92a	↑
	MiR-150	↓
DM	MiR-7,223	↓

Deng X, Su Y, Wu H, Wu R, Zhang P, Dai Y, et al. Scandinavian journal of immunology. 2015;81(3):153-65.

microRNAs in stem cell research



Navarro A, Monzó M. Yonsei medical journal. 2010;51(5):622-32.

microRNAs in stem cell research

In 2015 Zhou C et al

overexpression of pluripotency stem cell-specific miRNA-302/367 cluster, miRNA-9/9 and miRNA-124 induced fibroblasts conversion into neurons.

important implications : studies of neuron development and neurological disease therapy.(15)

microRNAs in stem cell research

In 2015 Möbus S et al

miR-199a-5p inhibition in ES-derived HLCs leads to improved hepatocyte differentiation.

Upon transplantation, HLCs were able to engraft and repopulate the liver of mice.

miRNA modulation may serve as a promising approach to generate more mature HLCs from stem cell sources for the treatment of liver diseases.(16)

microRNAs as biomarkers in plasma or serum

in 2008 first report

Chim et al

miRNAs as diagnostic tools in biological fluids

detected placental miRNAs in the maternal plasma(17)

in 2008 Lawrie et al

comparing serum from diffuse large B-cell lymphoma patients and healthy controls

miR-155, miR-210 and miR-21 levels were significantly upregulated in patients(18)

microRNAs as biomarkers in plasma or serum

in 2010 Murata et al

analyzed miRNAs plasma levels in rheumatoid arthritis

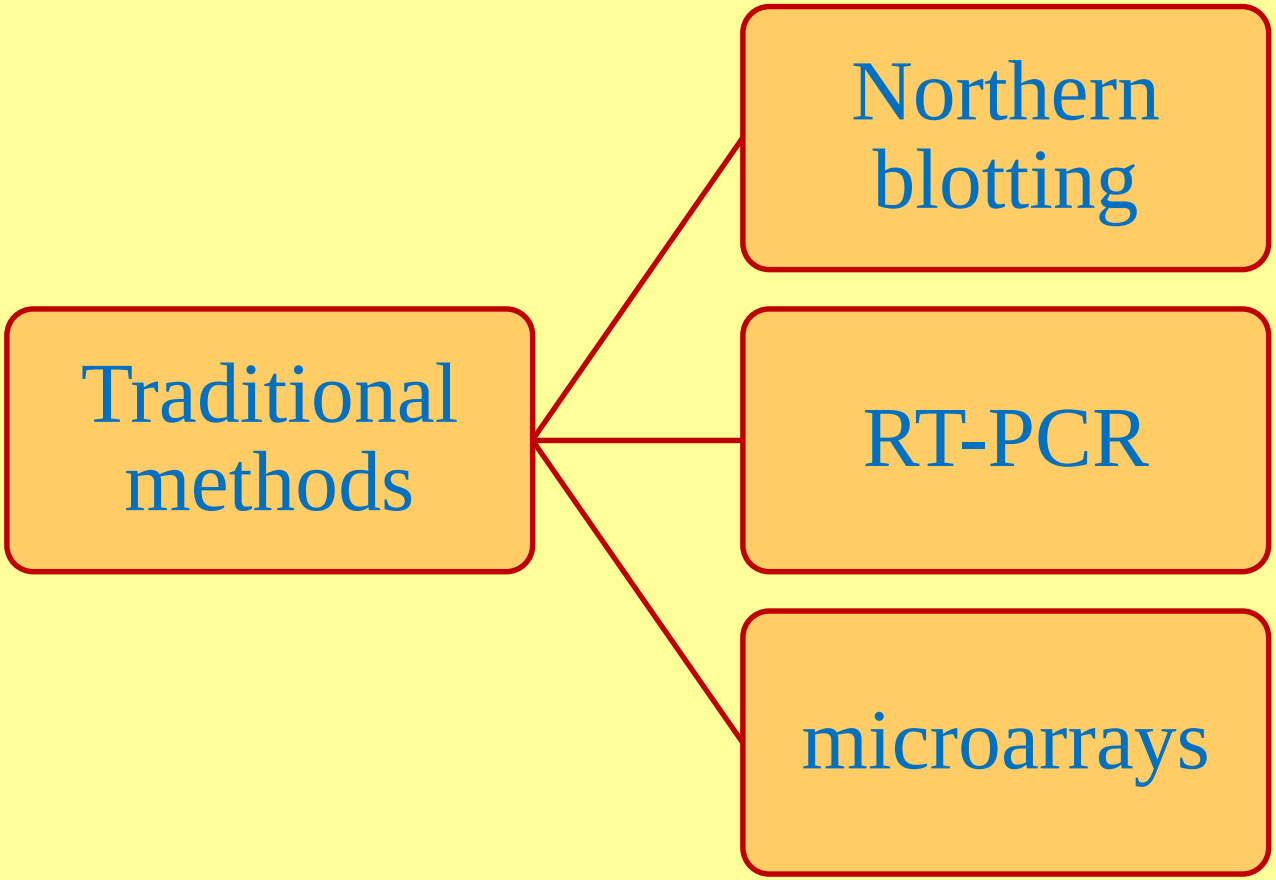
plasma miR-132 was significantly higher in healthy controls than in rheumatoid arthritis(19)

in 2015 Tsochandaridis et al

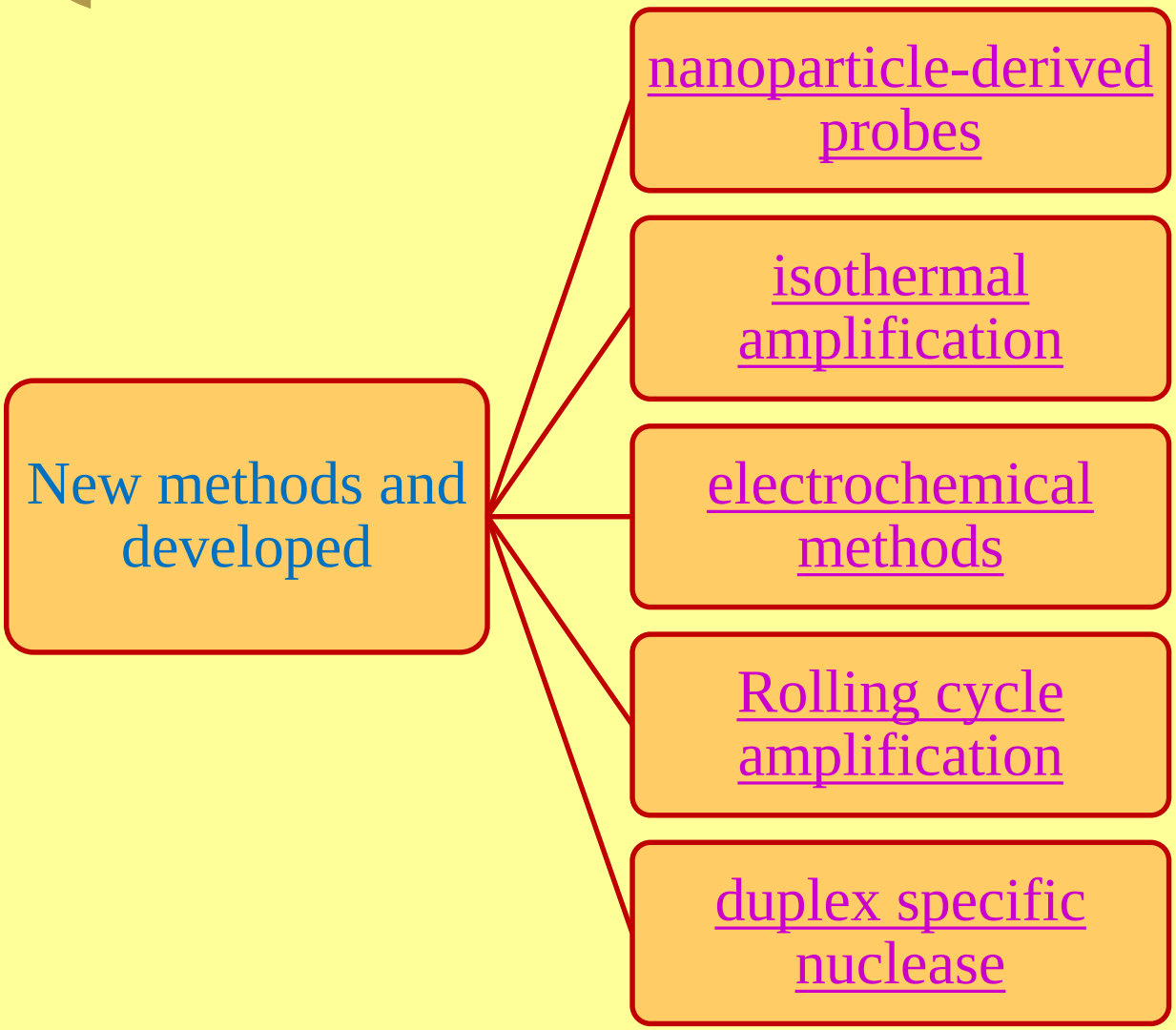
noninvasive diagnostic and prognostic biomarkers for pregnancy monitoring

prevent the development of gestational disorders and form the basis of personalized therapeutic strategies(20)

microRNA detection methods(21)



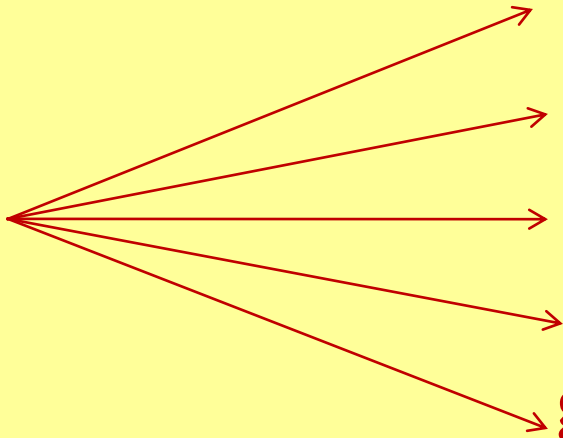
microRNA detection methods



nanotechnology and nanomaterials

- potent tools in bioanalysis
- detection of biological targets
- high sensitivity
- high efficiency

Nanoparticles



- gold nanoparticles
- silver nanoculsters
- magnetic particles
- quantum dots
- graphene oxide

AuNPs-based methods

- ✓ Simple probe design,
- ✓ easy modification,
- ✓ biocompatibility,
- ✓ easy cellular-uptake

Disadvantages

Specialized nanotechnology platform needed

Quantum dot-based methods

- ✓ Special fluorescence properties
- ✓ also easy modification
- ✓ simple design of probe
- ✓ easy cellular-uptake

Disadvantages
- Cell cytotoxicity
- unsuitable for multiple target detection

Isothermal exponential amplification

- ✓ No PCR needed
- ✓ good efficiency of signal amplification
- ✓ good sensitivity even low at the single cell level
- ✓ real-time assay in some cases

Disadvantages → Complicated probe design

Disadvantages → multiple enzymes

Presented by: Ghadimi
Under supervision: Dr. Ahmadpour

Some cleavage-based methods

- ✓ Simplified enzymatic system
- ✓ good sensitivity and selectivity
- ✓ less side reactions

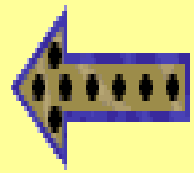
Disadvantages → Special enzymes needed

Rolling cycle amplification

- ✓ no PCR needed,
- ✓ good efficiency of signal amplification
- ✓ in situ detection achieved in some cases

Disadvantages

- Complicated probe design
- nonspecific amplification
- background
- more condition optimization needed



DSN and AuNPs-based system

- ✓ 0.2 fmol level detection
- ✓ simple design of probe

Disadvantages → Time consuming

Capillary-electrophoresis-based assay

- ✓ Simple probe design
- ✓ multiple target detection

Disadvantages

Specialized equipment need

Using bioinformatics tools to identify miRs

- KEGG: http:// www.genome.jp/kegg/
- Target Scan : http://www.targetscan.org/
- miRBase: http://www.mirbase.org/
- miRWalk: http://www.umm.uni-heidelberg.de/apps/zmf/mirwalk
- miRanda :http://www.microrna.org

Using bioinformatics tools to identify miRs

- Diana-microT: http://diana.cslab.ece.ntua.gr/
- TarBase: : http:// diana.cslab.ece.ntua.gr/
- miRDB : http:// mirdb.org/
- GEO: www.ncbi.nlm.nih.gov/gds
- miRNAMap: http://mirnamap.mbc.nctu.edu.tw/

KEGG ▼ Search Help

» Japan

KEGG Home
Release notes
Current statistics
Plea from KEGG

KEGG Database
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KEGG mapping
Color codes

KEGG Objects
Pathway maps
Brite hierarchies

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KegTools
KEGG API
KGML

KEGG FTP
Subscription

GenomeNet

DBGET/LinkDB

Feedback

Kanehisa Labs

KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (See Release notes for new and updated features).

New article - KEGG as a reference resource for gene and protein annotation

Main entry point to the KEGG web service

KEGG2	KEGG Table of Contents	Update notes

Data-oriented entry points

KEGG PATHWAY	KEGG pathway maps	[Pathway list]
KEGG BRITE	BRITE functional hierarchies	[Brite list]
KEGG MODULE	KEGG modules	[Module list | Statistics]
KEGG ORTHOLOGY	Ortholog groups	[KO system | Annotation]
KEGG GENOME	Genomes	[KEGG organisms]
KEGG GENES	Genes and proteins	[Release history]
KEGG COMPOUND	Small molecules	[Compound classification]
KEGG REACTION	Biochemical reactions	[Reaction modules]
KEGG DISEASE	Human diseases	[Cancer | Pathogen]
KEGG DRUG	Drugs	[ATC drug classification]
KEGG MEDICUS	Health information resource	[Drug labels search]

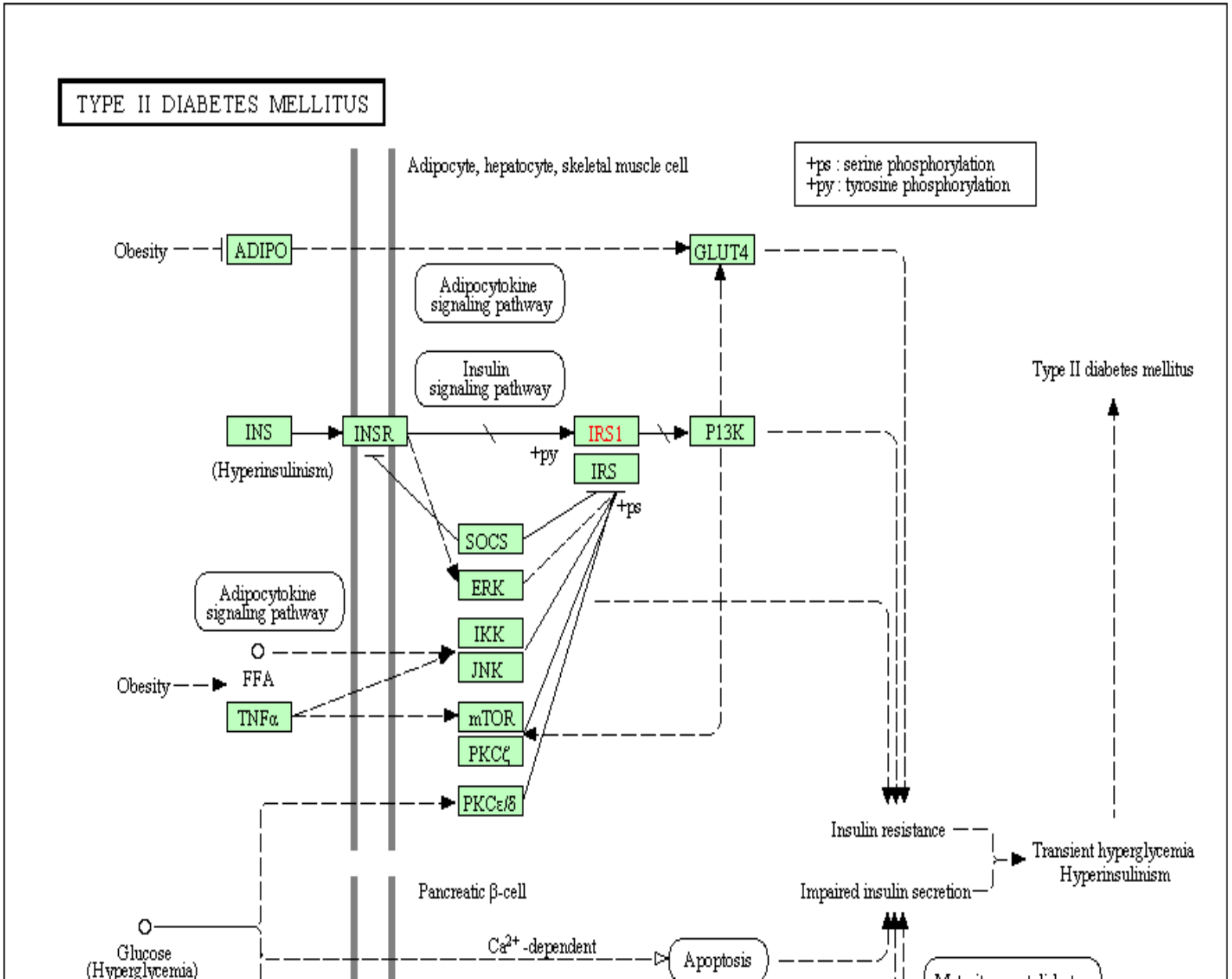
Organism-specific entry points

KEGG Organisms Enter org code(s) Go hsa hsa eco

KEGG Type II diabetes mellitus - Homo sapiens (human)

[Pathway menu | Organism menu | Pathway entry | Download KGML | Show description | User data mapping]

Homo sapiens (human) Go 100%



TargetScanHuman

Prediction of microRNA targets Release 7.0: August 2015 Agarwal *et al.*, 2015

Search for predicted microRNA targets in mammals

[Go to TargetScanMouse]
[Go to TargetScanWorm]
[Go to TargetScanFly]
[Go to TargetScanFish]

1. Select a species Human

AND

2. Enter a human gene symbol (e.g. "HMGA2")
or an Ensembl gene (ENSG00000149948) or transcript (ENST00000403681) ID

AND/OR

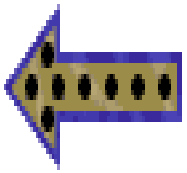
3. Do one of the following:

- Select a broadly conserved* microRNA family: Broadly conserved microRNA families
- Select a conserved* microRNA family: Conserved microRNA families
- Select a poorly conserved microRNA family: Poorly conserved microRNA families Note that many of these families are star miRNAs or small RNAs that have been misclassified as miRNAs.
- Enter a microRNA name (e.g. "miR-1-3p")

TargetScanHuman

Prediction of microRNA targets

Release 7.0: August 2015 Agarwal *et al.*, 2015



Human | miR-135-3p

100 transcripts with 1 sites, containing a total of 160 sites.

Top 100 predicted targets, irrespective of site conservation, ranked by cumulative weighted context++ score.

The table shows at most one transcript per gene, selected for being the most prevalent, based on 3P-seq tags (or the one with the longest 3' UTR, in case of a tie). [Download table]

Target gene	Representative transcript	Gene name	Number of 3P-seq tags supporting UTR + 5	Link to sites in UTRs	Site counts				6mer sites	Repre-sentative miRNA	Cumulative weighted context++ score	Total context++ score	Aggregate P_{CT}
					total	8mer	7mer-m8	7mer-A1					
ZNF791	ENST00000446165.1	zinc finger protein 791	242	Sites in UTR	5	0	0	5	5	hsa-miR-135a-3p	-1.43	-1.48	N/A
C15orf53	ENST00000318792.1	chromosome 15 open reading frame 53	5	Sites in UTR	3	0	3	0	0	hsa-miR-135a-3p	-0.83	-0.83	N/A
C4orf40	ENST00000344526.5	chromosome 4 open reading frame 40	5	Sites in UTR	3	1	2	0	0	hsa-miR-135a-3p	-0.82	-0.82	N/A
ZNF629	ENST00000262525.4	zinc finger protein 629	44	Sites in UTR	4	0	0	4	3	hsa-miR-135a-3p	-0.80	-0.80	N/A
ADO	ENST00000373783.1	2-aminoethanethiol (cysteamine) dioxygenase	686	Sites in UTR	2	1	1	0	0	hsa-miR-135a-3p	-0.78	-0.78	N/A
ZNF763	ENST00000343949.5	zinc finger protein 763	5	Sites in UTR	1	0	0	1	7	hsa-miR-135a-3p	-0.75	-0.75	N/A
AC069547.1	ENST00000595931.1	HCG1745369; PRO3073; Uncharacterized protein	5	Sites in UTR	1	1	0	0	0	hsa-miR-135a-3p	-0.74	-0.74	N/A
ANAPC5	ENST00000441917.2	anaphase promoting complex subunit 5	1380	Sites in UTR	1	1	0	0	1	hsa-miR-135a-3p	-0.73	-0.74	N/A
ZNF214	ENST00000278314.4	zinc finger protein 214	7	Sites in UTR	2	0	0	2	1	hsa-miR-135a-3p	-0.70	-0.70	N/A
UPK2	ENST00000264031.2	uroplakin 2	5	Sites in UTR	1	1	0	0	0	hsa-miR-135a-3p	-0.70	-0.70	N/A
PAPPA-AS1	ENST00000445861.2	PAPPA antisense RNA 1	5	Sites in UTR	2	0	2	0	0	hsa-miR-135a-3p	-0.70	-0.70	N/A
ZNF23	ENST00000497160.1	zinc finger protein 23	5	Sites in UTR	1	0	0	1	7	hsa-miR-135a-3p	-0.69	-0.69	N/A
KRT12	ENST00000251643.4	keratin 12	5	Sites in UTR	2	0	2	0	0	hsa-miR-135a-3p	-0.69	-0.69	N/A
LIN7C	ENST00000278193.2	lin-7 homolog C (C. elegans)	1701	Sites in UTR	3	0	1	2	0	hsa-miR-135a-3p	-0.68	-0.68	N/A

Latest miRBase blog posts

High confidence miRNA set available for miRBase 21 By sam (July 3, 2014)

As mentioned previously, we briefly held off from releasing the set of "high confidence" miRNAs for miRBase 21, because of a last-gasp bug. Those data are now available, tagged with the label "high confidence" on the entry pages, and for download on the FTP site. The total number of miRNAs labelled "high confidence" has increased [...]

miRBase 21 finally arrives By sam (June 26, 2014)

Apologies for the longer-than-usual wait. miRBase 21 is now available on the website, and all data available for download on the FTP site. As usual, the release notes describe the major changes. Of particular note this time, the Genome Reference Consortium have released a new human genome assembly, GRCh38. We have therefore remapped the human [...]

miRNA count: 28645 entries

Release 21: June 2014

Search by miRNA name or keyword

mir-135a Go Example

Download published miRNA data

Download page | FTP site

Tweets by @mirbase

miRBase: the microRNA database

miRBase provides the following services:

- The miRBase database is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for searching and browsing, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also available for download.
- The miRBase Registry provides miRNA gene hunters with unique names for novel miRNA genes prior to publication of results. Visit the help pages for more information about the naming service.

To receive email notification of data updates and feature changes please subscribe to the miRBase announcements mailing list. Any queries about the website or naming service should be directed at mirbase@manchester.ac.uk.

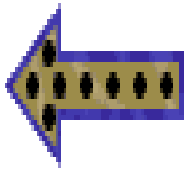
miRBase is managed by the Griffiths-Jones lab at the Faculty of Life Sciences, University of Manchester with funding from the BBSRC. miRBase was previously hosted and supported by the Wellcome Trust Sanger Institute.

Accession	ID	miRNA name	Previous ID	Mature name	Previous Mature ID
MI0000161	mmu-mir-135a-1	✓			
MI0000452	hsa-mir-135a-1	✓			
MI0000453	hsa-mir-135a-2	✓			
MI0000715	mmu-mir-135a-2	✓			
MI0000908	rno-mir-135a	✓			
MI0001169	gga-mir-135a-2	✓			
MI0001231	gga-mir-135a-1	✓			
MI0001264	gga-mir-135a-3	✓			
MI0002540	mml-mir-135a-2	✓			
MI0002541	ptr-mir-135a-2	✓			
MI0002542	ggo-mir-135a	✓			
MI0002543	ppy-mir-135a-2	✓			
MI0003388	fru-mir-135a	✓			
MI0003389	tni-mir-135a	✓			
MI0003692	dre-mir-135a	✓			
MI0005297	mdo-mir-135a	✓			
MI0006902	oan-mir-135a	✓			
MI0007624	mml-mir-135a-1	✓			
MI0008025	cfa-mir-135a-2	✓			
MI0008536	ptr-mir-135a-1	✓			
MI0009736	bta-mir-135a-2	✓			
MI0009737	bta-mir-135a-1	✓			

Search Results

Found **40** Homo sapiens miRNAs on chromosome chr13

Accession	ID	Chromosome	Start	End	Strand
MI0016862	hsa-mir-4499	chr13	20433778	20433846	-
MI0011282	hsa-mir-2276	chr13	24162416	24162504	+
MI0015835	hsa-mir-4305	chr13	39664034	39664135	-
MI0008190	hsa-mir-320d-1	chr13	40727828	40727875	-
MI0003635	hsa-mir-621	chr13	40810766	40810861	+
MI0014199	hsa-mir-3168	chr13	41101019	41101100	-
MI0017873	hsa-mir-5006	chr13	41568286	41568395	-
MI0025915	hsa-mir-8079	chr13	44196129	44196200	-
MI0016003	hsa-mir-3613	chr13	49996415	49996501	-
MI0000070	hsa-mir-16-1	chr13	50048973	50049061	-
MI0000069	hsa-mir-15a	chr13	50049119	50049201	-
MI0019300	hsa-mir-5693	chr13	51348567	51348639	-
MI0017336	hsa-mir-4703	chr13	51552589	51552667	+
MI0004065	hsa-mir-759	chr13	52810050	52810140	+
MI0006358	hsa-mir-1297	chr13	54311972	54312048	-
MI0017874	hsa-mir-5007	chr13	55174454	55174548	+
MI0014200	hsa-mir-3169	chr13	61199798	61199880	-
MI0016833	hsa-mir-548x-2	chr13	65966330	65966429	-
MI0017327	hsa-mir-4704	chr13	66218250	66218324	+



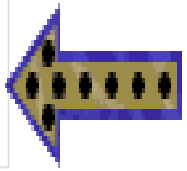
mRWalk 2.0: a comprehensive atlas of predicted and validated miRNA-target interactions

NEWS

miRWalk 2.0: a comprehensive atlas of predicted and validated miRNA-target interactions

- Gene-miRNA Targets
- MicroRNA-gene Targets
- Gene-miRNA-pathway Targets
- Gene-miRNA-GO Targets
- Gene Class Targets
- Cell line-based miRNAs
- Organ-based miRNAs
- miRNA-based search in organs
- Gene-miRNA-OMIM Targets
- Disease-ontology search
- Human Phenotype Ontologies
- **Disease-based miRNAs**
- Literature on miRNAs
- miRNA processing proteins

NEWS



microRNA.org - Targets and Expression

Predicted microRNA targets & target downregulation scores. Experimentally observed expression patterns.

August 2010 Release Last Update: 2010-11-01 [release notes]

target sites by: miRanda - scores by: mirSVR

Computational Biology Center: cBio@MSKCC

miRNA | Target mRNA | miRNA Expression | Downloads | FAQ

microRNA.org Releases:

- August 2010 release: http://www.microrna.org/
- September 2008 release: (for a limited time): http://cbio.mskcc.org/microrna-previous/
- 2005 release: http://cbio.mskcc.org/mirnaviewer/

You are currently searching:

- All Species

miRNA Stats:

- Homo sapiens: 1100
- Mus musculus: 717
- Rattus norvegicus: 387
- Drosophila melanogaster: 186
- Caenorhabditis elegans: 233

Other microRNA resources:

- PicTar
- TargetScan
- MicroCosm
- miRBase

miRNA Search

miRNA(s): miR-135a fuzzy search ("let-7" will match "let-7a", "let-7b", etc.)

Species: Homo sapiens

Go

mirSVR predicted target site scoring method: Comprehensive modeling of microRNA targets predicts functional non-conserved and non-

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miRNA | Target mRNA | miRNA Expression | Downloads | FAQ

You are currently searching:

- Homo sapiens
- miR-135a

miRNA Stats:

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- Rattus norvegicus: 387
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- Caenorhabditis elegans: 233

Searched for: miR-135a AND Homo sapiens

1 match select all clear all

miRNA	Genes Targeted	Links
hsa-miR-135a	7,414	[view targets] [view expression profile] [view in miRBase] [view in miRò]

[view mRNAs targeted by ALL selected miRNAs] [view expression profiles of ALL selected miRNAs]

mirSVR predicted target site scoring method: Comprehensive modeling of microRNA targets predicts functional non-conserved and non-

microRNA.org - Targets and Expression

Predicted microRNA targets & target downregulation scores. Experimentally observed expression patterns.

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target sites by: miRanda scores by: mirSVR

Computational Biology Center: cBio@MSKCC

You are currently searching:

- Homo sapiens
- hsa-miR-135a

[view targets]
[view expression profile]

miRNA Stats:

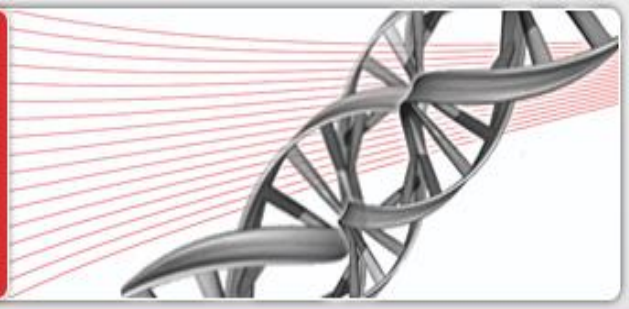
- Homo sapiens: 1100
- Mus musculus: 717
- Rattus norvegicus: 387
- Drosophila melanogaster: 186
- Caenorhabditis elegans: 233

Selected miRNAs: hsa-miR-135a

Click ⊞ to view alternative isoforms.

Displaying results 1 - 50 of 7,414
first | next | last

mRNAs Targeted by hsa-miR-135a			mirSVR score
C9orf82	hsa	NM_024828,AK300739 [alignment details]	-2.97
⊞ B3GALTL	hsa	NM_194318,BX647932 [alignment details]	-2.60
⊟ MYNN	hsa	NM_018657,AB079778,AF148848,AF155508,AK304281 [alignment details]	
For this gene, only alternative isoforms met search criteria			
		AY514901 [alignment details]	-2.59
TSPAN31	hsa	NM_005981,AK294128,BX647402 [alignment details]	-2.56
MAN2A1	hsa	NM_002372 [alignment details]	-2.33
⊟ SUN1	hsa	NM_025154,NM_001130965,AK025737,AK302896,AK304150,BX648893... [alignment details]	
For this gene, only alternative isoforms met search criteria			
		AK022469 [alignment details]	-2.27
⊟ MFN1	hsa	NM_033540,AB043588,U95822 [alignment details]	
For this gene, only alternative isoforms met search criteria			
		AK000700 [alignment details]	-2.18
⊞ GULP1	hsa	NM_016315,AK298626,AK314498,BC068525 [alignment details]	-2.17
⊞ LCOR	hsa	NM_032440,AB058698,AL832106 [alignment details]	-2.11
⊞ FAM72D	hsa	NM_207418 [alignment details]	-2.09



IMPORTANT NOTE:
This site is no longer supported. The **new and improved Web interface** can be accessed through here.

WELCOME TO THE DIANA LAB WEBPAGE

Lab Intro

Computational predictive models are a key element of current systems biology. The focus of the DIANA lab is on the development of algorithms, databases and tools for interpreting and archiving genomic data in the framework of a systemic analysis. Current emphasis is on the analysis of microRNA (miRNA) and protein coding genes. MiRNAs are recently identified to be very abundant in mammalian organisms and play a key role in regulating development.

Comprehensive models work and integrate data at various levels of biological detail. Therefore the activities of the DIANA lab range from the analysis of expression regulation from deep sequencing data, the annotation of miRNA regulatory elements and targets to the interpretation of the role of miRNAs in various diseases.

Currently active projects of the DIANA-lab group include:

MicroRNA target prediction

DIANA-microT-CDS (v5.0): DIANA-microT-CDS is the 5th version of the microT algorithm. It is specifically trained on a positive and a negative set of miRNA Recognition Elements (MREs) located in both the 3'-UTR and CDS regions. DIANA-microT-CDS provides a significant increase in sensitivity compared to the previous version (65% vs 52%), when compared against experimental proteomics data. It exhibited the highest sensitivity at any level of specificity, when compared against other state of the art implementations. DIANA-microT-CDS has been updated (July 2012) to miRBase 18 and is fully compatible with the new miRNA nomenclature introduced in this version. It also provides hyperlinks to on-line servers such as iHOP and expression data for the selected

TarBase v.5c Latest version of TarBase HERE Download TarBase

MORE RECENT VERSION OF TARBASE AVAILABLE!

The **new and improved web interface** containing **updated data** can be accessed through here.

If used, please cite: The database of experimentally supported targets: a functional update of TarBase. (Papadopoulos GL, Reczko M, Simossis VA, Sethupathy P, Hatzigeorgiou AG.), Nucleic Acids Res. 2009 Jan;37(Database issue):D155-8. Epub 2008 Oct 27.

For issues regarding this application contact **maragkakis[at]fleming.gr**

Select properties in the fields if you want to restrict your query | Toggle More Options (on/off) | Start a new search

Human ▾ Any miRNA ▾ HIC ▾

Target Search

Target Mining

Custom Prediction

FuncMir Collection

Data Download

Statistics

Help | FAQ

Comments

Citation | Policy

Choose one of the following search options:

Search by miRNA name

Human | Go | Clear

Search by gene target

Human | Gene Symbol | Go | Clear

miRDB is an online database for miRNA target prediction and functional annotations. All the targets were predicted by a bioinformatics tool, MirTarget, which was developed by analyzing thousands of miRNA-target interactions from high-throughput sequencing experiments. Common features associated with miRNA target binding have been identified and used to predict miRNA targets with machine learning methods. miRDB hosts predicted miRNA targets in five species: human, mouse, rat, dog and chicken. As a recent update, users may provide their own sequences for customized target prediction.

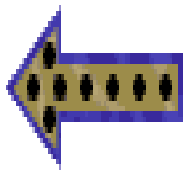
Reference:

Nathan Wong and Xiaowei Wang (2015) miRDB: an online resource for microRNA target prediction and functional annotations. Nucleic Acids Research. 43(D1):D146-152.

miRDB

There are 158 predicted targets for hsa-miR-135a-3p in miRDB.

Target Detail	Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
Details	1	98	hsa-miR-135a-3p	GLYCTK	glycerate kinase
Details	2	96	hsa-miR-135a-3p	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta
Details	3	95	hsa-miR-135a-3p	CHD6	chromodomain helicase DNA binding protein 6
Details	4	92	hsa-miR-135a-3p	EP300	E1A binding protein p300
Details	5	90	hsa-miR-135a-3p	RHOBTB3	Rho-related BTB domain containing 3
Details	6	89	hsa-miR-135a-3p	PAIP1	poly(A) binding protein interacting protein 1
Details	7	89	hsa-miR-135a-3p	QSER1	glutamine and serine rich 1
Details	8	88	hsa-miR-135a-3p	COA6	cytochrome c oxidase assembly factor 6 homolog (S. cerevisiae)
Details	9	88	hsa-miR-135a-3p	FANCF	Fanconi anemia, complementation group F
Details	10	88	hsa-miR-135a-3p	VEZF1	vascular endothelial zinc finger 1
Details	11	87	hsa-miR-135a-3p	XG	Xg blood group
Details	12	85	hsa-miR-135a-3p	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)
Details	13	84	hsa-miR-135a-3p	PTBP3	polypyrimidine tract binding protein 3
Details	14	84	hsa-miR-135a-3p	LCP1	lymphocyte cytosolic protein 1 (L-plastin)
Details	15	84	hsa-miR-135a-3p	ZBTB41	zinc finger and BTB domain containing 41
Details	16	83	hsa-miR-135a-3p	TFE3	transcription factor binding to IGHM enhancer 3
Details	17	83	hsa-miR-135a-3p	HIRA	histone cell cycle regulator
Details	18	82	hsa-miR-135a-3p	ZKSCAN1	zinc finger with KRAB and SCAN domains 1
Details	19	82	hsa-miR-135a-3p	C15orf53	chromosome 15 open reading frame 53
Details	20	82	hsa-miR-135a-3p	GAB1	GRB2-associated binding protein 1
Details	21	81	hsa-miR-135a-3p	ARL14	ADP-ribosylation factor-like 14
Details	22	79	hsa-miR-135a-3p	RERG	RAS-like, estrogen-regulated, growth inhibitor
Details	23	79	hsa-miR-135a-3p	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)
Details	24	78	hsa-miR-135a-3p	ZSWIM6	zinc finger, SWIM-type containing 6
Details	25	77	hsa-miR-135a-3p	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein



Gene Expression Omnibus

GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.

Gene Expression Omnibus

mir-135a Search

There are 27 results for "mir-135a" in the GEO DataSets Database.

There are 2 results for "mir-135a" in the GEO Profiles Database.

Getting Started

- Overview
- FAQ
- About GEO DataSets
- About GEO Profiles
- About GEO2R Analysis
- How to Construct a Query
- How to Download Data

Tools

- Search for Studies at GEO DataSets
- Search for Gene Expression at GEO Profiles
- Search GEO Documentation
- Analyze a Study with GEO2R
- GEO BLAST
- Programmatic Access
- FTP Site

DataSets:	3848
Series:	62415
Platforms:	15114
Samples:	1613398

Information for Submitters

- Login to Submit
- Submission Guidelines
- Update Guidelines
- MIAME Standards
- Citing and Linking to GEO
- Guidelines for Reviewers

miRNAMap

Home | About | Browse | Search | Statistics | Downloads | Tutorial

keyword in ◉ microRNA or ○ target gene : Homo sapiens ▾ [ ] Search Example

Welcome to miRNAMap!

What's new?

- More species
- More prediction tools
- Gene group search
- miRNA target accessibility
- faster and More comprehensive

Release 2.0 : July 2007

miRNAMap Previous version - miRNAMap 1.0

mature miRNA count:

Homo sapiens	542
Mus musculus	424
Danio rerio	371
Rattus norvegicus	261
Xenopus tropicalis	196
Gallus gallus	162
Caenorhabditis elegans	135
Fugu rubripes	133
Monodelphis domestica	111
Drosophila melanogaster	85
Anopheles gambiae	38
Canis familiaris	6

Citing miRNAMap2:
Hsu SD, Chu CH, Tsou AP, Chen SJ, Chen HC, Hsu PW, Wong YH, Chen YH, Chen GH, Huang HD (2008) 'miRNAMap 2.0: genomic maps of microRNAs in metazoan genomes.' Nucleic Acids Res. 2008 Jan;36(Database issue):D165-9. [Pubmed]

miRNAMap

Home | About | Browse | Search | Statistics | Downloads | Tutorial

keyword in ◉ microRNA or ○ target gene : Homo sapiens ▾ Search Example

Browse

The advancements and new features miRNAMap 2.0.

Features	miRNAMap 1.0	miRNAMap 2.0
Known miRNAs	miRBase (version 6.0)	miRBase (version 9.2)
Supported species	human, mouse, rat and dog	2 insects, 9 vertebrates and 1 worm
Experimental miRNA targets	Surveying literature	TarBase and Surveying literature
miRNA expression profiling	Lu. et al miRNA profiling in human	Lu. et al miRNA profiling in human Q-PCR miRNA profiling in human
Expression profiles of miRNA targets	-	NCBI-GEO-GDS596 (76 human tissues)
miRNA target prediction tools	miRanda	miRanda, RNAhybrid and TargetScan
Criteria for filtering the predicted miRNA targets	-	Criterion 1: *predicted by at least two tools* Criterion 2: *target genes contained multiple sites* Criterion 3: *target site is accessible*
Accessible region of miRNA target sites	-	Sfold
Tissue specificity of human miRNAs	-	Q-PCR miRNA profiling (18 human tissues)

Items 1-2 of 2 displayed.

Show: 20 Page 1 of 1

Download Results (Excel format)

ID	Species	Locate on chromosome	Locate on gene exon/intron/UTR	Get seq
hsa-mir-135a-1	Homo sapiens	3 : 52303275-52303364 : -	OTTHUMT00000264972 (intron)	
hsa-mir-135a-2	Homo sapiens	12 : 96481721-96481820 : +	OTTHUMT00000262257 (intron)	
				Select ALL

Get miRNA's sequence: Mature sequence Fetch Sequences Reset


تقدیم برای عرض تشکر

References

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